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I, KIM MARSHALL, MANAGER EXAMINATION SUPPORT AND SALES,  
hereby certify that the annexed is a true copy of the Provisional specification in  
connection with Application No. PP 2264 for a patent by CSL LIMITED filed on  
10 March 1998.

## PRIORITY DOCUMENT

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KIM MARSHALL  
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AUSTRALIA

Patents Act 1990

CSL LIMITED

PROVISIONAL SPECIFICATION

*Invention Title:*

*Porphyromonas gingivalis probes and polypeptides*

The invention is described in the following statement:

*Porphyromonas gingivalis* probes and polypeptides

FIELD OF THE INVENTION

5           The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*.

BACKGROUND OF THE INVENTION

10           Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated  
15 with a subgingival infection of a consortium of specific Gram-negative bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is *P. gingivalis* as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically  
20 cultivable flora, whereas *P. gingivalis* is rarely recovered, and then in low numbers, from healthy sites. A proportional increase in the level of *P. gingivalis* in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of  
25 the disease. The progression of periodontitis lesions in non-human primates has been demonstrated with the subgingival implantation of *P. gingivalis*. These findings in both animals and humans suggest a major role for *P. gingivalis* in the development of adult periodontitis.

*P. gingivalis* is a black-pigmented, anaerobic, asaccharolytic,  
30 proteolytic Gram-negative rod that obtains energy from the metabolism of specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III) oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence  
35 factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

In order to develop an efficacious and safe vaccine to prevent *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens to generate neutralising antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis* this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets:

It is also well known that *P. gingivalis* produces a range of broadly active proteases (University of Melbourne International Patent Application No PCT /AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

## SUMMARY OF THE INVENTION

The present inventors have attempted to isolate *P. gingivalis* nucleotide sequences which can be used for recombinant production of *P. gingivalis* polypeptides and to develop nucleotide probes specific for *P. gingivalis*. The DNA sequences listed below have been selected from a

large number of *P. gingivalis* sequences according to their indicative potential as vaccine candidates. This intuitive step involved comparison of the deduced protein sequence from the *P. gingivalis* DNA sequences to the known protein sequence databases. Some of the characteristics used to select useful vaccine candidates include; the expected cellular location, such as outer membrane proteins or secreted proteins, particular functional activities of similar proteins such as those with an enzymatic or proteolytic activity, proteins involved in essential metabolic pathways that when inactivated or blocked may be deleterious or lethal to the organism, proteins that might be expected to play a role in the pathogenesis of the organism eg. red cell lysis, cell agglutination or cell receptors and proteins which are paralogues to proteins with proven vaccine efficacy. DNA sequences that were considered to be poor vaccine candidates and not selected include those that code for proteins involved in replication, non-essential proteins involved in cellular processes and those proteins present at sites that would be unlikely to be affected by immune mediators such as those found in the bacterial cytoplasm or inner membranes.

In a first aspect the present invention consists in an isolated *P. gingivalis* nucleotide sequence, the nucleotide sequence consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37 and sequences complementary thereto.

In a second aspect the present invention consists in an isolated *P. gingivalis* polypeptide, the polypeptide being at least partially encoded by a nucleotide consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID

NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24,  
 SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO:  
 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID  
 NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37 and sequences  
 5 complementary thereto.

In a third aspect the present invention consists in a nucleotide probe  
 specific for *P. gingivalis*, the probe including a detectable label and a  
 nucleotide sequence of at least 15 nucleotides, the nucleotide sequence  
 being derived from a sequence selected from the group consisting of SEQ ID  
 10 NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID  
 NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID  
 NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16,  
 SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID  
 NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25,  
 15 SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID  
 NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34,  
 SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37 and sequences  
 complementary thereto.

20 Throughout this specification, unless the context requires otherwise,  
 the word "comprise", or variations such as "comprises" or "comprising", will  
 be understood to imply the inclusion of a stated element or integer or group  
 of elements or integers but not the exclusion of any other element or integer  
 or group of elements or integers.

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#### DETAILED DESCRIPTION

Preparation of the *P. gingivalis* library for sequencing.

30 To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated  
 from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method  
 described by Mamur J. (1961). Cloning of DNA fragments was performed  
 essentially as described by Fleischmann *et al.*, (1995). Briefly, purified  
 genomic DNA from *P. gingivalis* was nebulized to fragment the DNA and  
 35 was treated with Bal31 nuclease to create blunt ends then run twice on  
 preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from

the gel and the DNA recovered. This DNA was then ligated to the vector pUC18 (*Sma*I digested and dephosphorylated; Pharmacia) and electrophoresed on a 1% agarose preparative gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the library DNA and plated out on SOB agar antibiotic diffusion plates containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

#### 15 DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 96 well gridded array and stored at -20°C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems).

The sequences obtained are set out below.

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#### DNA sequence analysis

Raw trace data files from the ABI 377 sequencer were manually trimmed using Staden Pregap (Laboratory of Molecular Biology, Medical Research Council, UK) running on a Sun Microsystem computer. Trimmed files were assembled into contigs using Staden Gap v4.1 and exported as a consensus file in FastA format. This consensus was converted into GCG

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format files and analysed for homology using the FASTX algorithm on a non-redundant protein database compiled by ANGIS (Australian Genomic Information Service, University of Sydney). Individual FASTX search results were examined for significant homology by statistical probability and amino acid alignments.

The results are set out in Table 1.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this 9th day of March 1998

**CSL LIMITED**

Patent Attorneys for the Applicant:

**F.B. RICE & CO.**



**References.**

Mamur, J. (1961) A procedure for the isolation of deoxyribonucleic acid from micro-organisms. J. Mol. Biol. 3, 208-218.

Fleishmann, R.D. et al. (1995) Whole genome random sequencing and assembly of *Haemophilus influenzae* Rd. Science 269, 496-512.

Table 1

Contig #	SEQ ID NO.	Homology description	Accession number	% identity	Overlap (aa)	Statistical expectation
1363	1	Outer membrane integrity protein, Haemophilus influenzae	P71397	38.3	269	5.30E-34
1448	2	Outer membrane protein P64K or PM-6, Neisseria meningitidis	Q51189	44.8	116	1.20E-14
1506	3	Heat shock protein HTPG, Actinobacillus actinomycetemcomitans	G862902	34.3	458	1.40E-50
1534	4	HemB, Porphyromonas gingivalis	P95494	33.6	116	2.00E-11
1976	5	Zinc protease, Escherichia coli	G535004	28.3	272	9.30E-21
2073	6	Membrane fusion protein mtrC, Haemophilus influenzae	G64100	23.6	152	7.00E-07
2080	7	Outer membrane protein A, Escherichia fergusonii	G146991	52.5	59	1.30E-08
2152	8	Heat shock protein HSLU, Haemophilus influenzae	U32731	45	111	3.20E-14
2159	9	63kD protein, Bacteroides gingivalis	AB004560	32	382	5.50E-48
2307	10	Adhesin protein, Synechocystis sp.	D90903	30.1	229	5.00E-10
2389	11	Internalin A, Listeria monocytogenes	M67471	40.1	212	2.50E-21
238	12	Outer membrane protein X precursor, Vibrio cholerae	Q07023	29.1	172	5.30E-05
2425	13	Amylovoran export outer membrane protein AMSH, Erwinia amylovora	G600428	34.4	151	6.10E-06
2802	14	Outer membrane protein MIP, Legionella oakridgensis	G2231734	49.8	201	6.50E-37
2847	15	Hemin permease, Yersinia enterocolitica	G541768	32.6	141	3.20E-12
3064	16	Protease, Helicobacter pylori	G2314520	29.2	144	1.10E-11
3093	17	Thiol protease/hemagglutinin prtT precursor, Porphyromonas gingivalis	M8309	24.9	225	6.90E-09
3300	18	Hemolysin, Synechocystis sp.	D90914	22.6	283	1.30E-10

**Table 1**  
(cont.)

Contig #	SEQ ID NO.	Homology description	Accession number	% identity	Overlap (aa)	Statistical expectation
3589	19	Hemolysin A, <i>Prevotella melanogenica</i>	U27587	64.2	67	4.50E-15
3655	20	Internalin A, <i>Lysteria monocytogenes</i>	M67471	39.3	300	1.10E-34
3772	21	Heme uptake protein A, <i>Bacteriodes fragilis</i>	X97122	85.3	224	2.60E-90
3782	22	Arg-gingipain-1 proteinase, <i>Porphyromonas gingivalis</i>	U15282	39.9	143	1.40E-15
4041	23	Trypsin-like protease prtT, <i>Porphyromonas gingivalis</i>	A49228	69.2	39	8.50E-04
4174	24	36kD antigen, <i>Helicobacter pylori</i>	U86610	36.4	162	2.70E-19
4188	25	Polar flagellar protein, <i>Vibrio parahaemolyticus</i>	U12816	41.1	175	9.10E-18
4216	26	Trypsin-like protease prtT, <i>Porphyromonas gingivalis</i>	A49228	53	68	1.10E-06
4381	27	Hemagglutinin, <i>Prevotella intermedia</i>	AF017417	50	186	9.80E-33
4381	27	Abortive phage resist. Protein, <i>Lactococcus lactis</i>	U94520	39.5	124	8.00E-12
4413	28	DNA K heat shock protein, <i>Borrelia burgdorferi</i>	M96847	67.8	233	1.10E-68
4424	29	Heme A uptake protein, <i>Bacterioides fragilis</i>	X97122	69.9	171	8.20E-47
4426	30	36kD antigen, <i>Helicobacter pylori</i>	U86610	38.1	110	8.20E-11
4457	31	Outer membrane protein P4 precursor, <i>Haemophilus influenzae</i>	A43604	33.9	254	5.00E-23
4538	32	Polar flagellar protein, <i>Vibrio parahaemolyticus</i>	U12816	50.6	218	3.50E-44
4729	33	Outer membrane protein P64K or PM-6, <i>Neisseria meningitidis</i>	X84696	32	200	7.10E-15
4763	34	Hemolysin or CLPB protein, <i>Serpulina hyodysenteriae</i>	X73140	59.3	145	1.90E-24
496	35	Hemolysin, <i>Serpulina hyodysenteriae</i>	Q54318	37.8	156	3.50E-21
723	36	Protease, <i>Helicobacter pylori</i>	G2314520	46.7	139	7.40E-22
933	37	Hemolysin or CLPB preotein, <i>Serpulina hyodysenteriae</i>	Q54316	47.7	388	3.70E-75

## (2) INFORMATION FOR SEQ ID NO:1

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 885 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

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acgaatggga agaggggcac gatcgctacc agccatcgtc aaagaatgca atctggatgc    180
aaaagaaatc gtagccaaat ttctgcagcc cgggtattgtg ggtcttggcg gtgctacctt    240
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## (2) INFORMATION FOR SEQ ID NO:2

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 548 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...548
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

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gacttaaa						548

## (2) INFORMATION FOR SEQ ID NO:3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2309

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

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cgggaaaaat	gcttacaatc	cgaagatcag	aatgaaaaga	tagacgccgg	gaatacgaag	2220

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(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

gcacatttcc	gctgaagcta	agattgttag	ttgcataata	ggaaagcgat	ggcttacacc	60
ctgattttcc	tgtgcacgaa	aagtttttct	atacgtttct	ccaagaccgg	ttcgccggat	120
ccttttttct	tttttatttc	gaacggatat	tctgccagcc	atccgtatgg	tagaagaaat	180
agttggtatt	gctactaact	taccgatgtt	tatatcgagc	gaagtattgg	tttgccgatc	240
gttgctctcg	atatgcgatg	tgacgtatat	gcactcagtc	gattcgtatt	ctttttgtga	300
tcacattgat	taccccggcg	atggcatcgg	atccgtagag	cgactcgaag	cacctttcac	360
cagttcgatc	cgttcgatct	gatcaggaga	aaacgactca	aatcggcctg	accgcctaca	420
tcgccgtaca	cacgcttacc	acgataagga	tgaggatata	cttactgcta	aggccgntca	480
gctgcatgaa	gagcccatca	gattggggcc	gaagtcaaaa	gacggactca	gccctgcata	540
ggcctcggaa	gtaggagccg	agaaagaggg	tatgtcctta	gcggtaagac	tt	592

(2) INFORMATION FOR SEQ ID NO:5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

gggtaacgac	agcattcttc	accggatcga	tcatttgggg	aatagcctgt	tgaatgcttc	60
cagaggaacc	tgaggagcaa	aagcattcac	cgtctgattt	ccacctcaat	acccgggata	120
tagccgccat	cggtgaagta	ggtggagatt	cattggcata	agcattgttc	ttacgcttgt	180
ctctttcggt	gtattgttct	cgtatcgctt	gagcacattc	gngccgtgca	cgatccgtat	240
tcgccttggt	gaataccgaa	ctgacggagg	ctttctatct	ctgccaccaa	tgcgtcatcg	300
ctttctccgc	ttcaccctca	cgaaccgagg	caacaaaatt	gaagcgtcct	tagtctgggt	360

atgtacatg	aagttagaga	agaaagctcc	tgactgagga	aaggagcgtt	aggcttgtga	420
taaatctcgg	acagacgctc	atcacggctg	tagtgatcac	ctgtttcata	tagtcttcca	480
aagtccgaa	atcgatcctc	gcacttcttg	aggagtgggg	tcgctcttga	agctgatggg	540
agctgcgtgg	tagtagcctc	agcatcggtg	gcaatggcta	cgataggcca	tcgttgcctc	600
ctaccggcgt	atagatacgc	tctgctggat	tcacggggca	ggaacgctct	tgaagagttc	660
tttgatcttg	ttctccacat	agtccaatcg	atatctccca	cgatcaccag	accttgcagg	720
tcgggacgat	accattctta	taatagttgc	gcagctcatc	atgcttgaag	ttgagcacga	780
cgatcatcaga	ccgatgggca	tgcgttctgc	atatttatta	cccggcatag	cctggcaagt	840
atagcctcga	acatacgaag	gttggcatcg	cgacgagcac	gcactcttcc	tggatcacac	900
cgcgctcctc	gtcgatctca	tgcccgtcga	ggtaaatattg	ttactccaat	catgcaggat	960
aagcaagcg						969

## (2) INFORMATION FOR SEQ ID NO:6

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...729

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

cgaagaagat	ctgcaagccg	gcgaggacta	ccaatatgcc	gtggagggcg	caggctcgtc	60
atggaacggc	agcggcagga	ttcgctctac	agggggatca	ggtgcggcag	atggaggaga	120
gcctccataa	tatgcgtcgc	aatctgggat	ggtgcgcgcc	cgtgtggaag	acctgaacgt	180
gaaggcaccg	gccgacgtca	gttggggctt	ttggacgtgg	agatagggca	gacggtagga	240
gccggagtcg	catcggacag	atcaacgtcc	tgtccgacta	caaggtggag	gctagataga	300
cgagcactat	atcgatcggg	tcaaagccgg	tctggccgct	tcgtcgaacg	gcagggcagg	360
gacttctccc	ttcgcgttcg	gaaggtatac	ccgaagttcg	ggacaagcag	ttccgcaccg	420
acttcatatt	cgacggagag	cacccgacaa	tatccgcaca	ggccaaactt	actacatcaa	480
tctgcgcctc	gacagccgtc	cgaagccatc	atgatcccg	gcggagcctt	ctatcagaaa	540
ccggcggacg	atggatatcc	gtcggtacgc	ccgacggcaa	gcgagccgtc	gccgggacat	600
cacgattgcc	cgtcagaatc	gcgagtatta	cgaagttcct	ccggcctgca	ttgccgncga	660
gatggtcac	acctttcgta	tgatattccg	cgatgcataa	gaaattatcc	tgaatgaccc	720
acctatagc						729

## (2) INFORMATION FOR SEQ ID NO:7

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...500

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

gatttttctg	aaaccactag	tagatttttc	tgaaactaat	atcagattca	cgtactgaaa	60
aattaagtct	tatcaaagca	cacttggtac	ggctttgacg	ctctactttt	cattccacga	120
gcgattaacg	caactcttct	tcgatcaacg	gaactcggta	cgacggttca	gttggtcgca	180
gactgactgc	tgctcccggg	caaagggtgct	acgaattcct	cggtgagcac	atcgcttcc	240
ttcagaaatc	gtgccgttcg	gcaattttgg	ctgtcaccgt	cttggggaca	gactaccgta	300
gcctttccac	gtaagcctgt	cggccgctat	gccacgactc	gtgggtaatc	caccacggat	360
ttggctctgc	ggtcagatag	tccgaggttg	tagcatcggg	gcctttcctg	tcggcatgcg	420
aacccaattc	gatccgaata	tccgattgtc	cgtgaggata	cgaaatcagt	tcgtccaagc	480
tcttcatgct	ttcgggcgaa					500

## (2) INFORMATION FOR SEQ ID NO:8

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1169

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

ttcgccaactt	gacatcacgc	gtaatcgaag	gattatcact	cttacgggca	tcttgtctat	60
ctcatcgata	aagacaatcc	ctctctcggc	ctgtttgaat	cgtagtctgc	ggcctgcaaa	120
agtctgggtga	gaatactctc	aatgtctccc	ccacatagcc	ggcttcggtc	agtaccgtag	180
cgtcgactac	ggcgaaggaa	catggagcat	tttggtctac	gtacgagcca	agagtgtctt	240
gccgggtccc	tgggaccgac	cataataata	ttgcttttct	cgatctctac	gccacgctgt	300
cctcttgctg	gagcaatcgt	ttgtaatgat	tgtatacagc	gacgaaagaa	aacgtttggc	360
atcatcctgc	ccgataacat	acgaatcgag	aattccttga	tctctatagg	ccgaggcaag	420
tctctctctc	tcagattggt	ctctcttccg	atttgaattt	ttgcaatgct	tctcgaacca	480
cctctcctgc	cggagagcac	attcatcgca	gatatgagca	tggactcctt	cgagcatcag	540
tttacctgcg	ttctcggcat	gccacaaaaa	ctacagtatt	cttcgtcctt	ttctttgcca	600
tgagaaatat	acagtccccc	tttgggtaac	gagagggtac	tttcgattct	tttcgaggat	660
tttatctatc	atcccgtact	ccaatgttcg	ggggctgtca	tccaatagtc	ccgatcacta	720
tctttttcga	cctgccgacg	ggctttccac	tgtgagaaga	gataatcgtg	taaagctctt	780
tcttacgcgc	agaatctcgc	gagctgcgat	ctccaaatcg	ctggcctgcc	cctcatacca	840
ccaagcggct	gatgtatcat	cacgcgggaa	tgaggcaaag	caagcgtttg	cctttcgttc	900
ctgctacgag	cagcactgat	gccatagacg	cgccatgccc	gtacagatag	tggccacatc	960
gcaccctata	tactgcatcg	atcgtatatg	ccataaccgg	cataaacaga	tccgccgggt	1020
gaattcagaa	gatggaaata	tctttaccgg	ggtcggcgct	atcaagataa	agaagctggc	1080
ttgaatgaca	ttggccgtgt	aatcgtcgat	ctgagtgcc	aggaagagat	ccgatccatc	1140
attagacgtg	agaacacatc	catttgctgc				1169

## (2) INFORMATION FOR SEQ ID NO:9

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1144 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

cgttacactt	tcagggaaat	acttaagggt	cgtattcaga	gcaaacaaag	ctcttggtgc	60
ccctcaggat	aagacattgc	cacacgggtac	atttcggctc	actaagttct	ttcggagcag	120
tcttaatgat	ttcacgagct	tcttcgaggt	ataatcacga	acgatatacc	ccatgggtat	180
cgtattgcga	cgaaatcgg	atagatctga	tccaagatat	aacgataaga	cgaaagttgc	240
ttcaggcctg	ttcacgtgca	tcatcatcgg	catatttatc	ggagttgatt	atctcaatac	300
gcggtcacga	tcggctatat	cactcttttc	gatagccagt	ttcgccccctt	ccaatcttca	360
ccgccgaatt	cagtgggtat	attcgggcaat	gtttgccata	cttacgcacc	aattcttccg	420
cgagtctttt	agcacggcgc	tcgacaaagc	cttattgtgg	gctattgaag	cctcgggaga	480
agcaaaccct	cgatgatcat	tttattgacc	gaatagtttg	gattagcctt	aacggtgcta	540
caaattcttt	gattttctct	aactccgcct	tattgttgcg	atactcagaa	ggacatctgc	600
cttattgact	ttgaagttga	tataagcatc	gaagctgact	ctcgctgttt	ttccacttct	660
tctgccggag	taatgtgtgc	cancaataag	gagcctctgc	cggattgaag	agtggatcaa	720
aaggancaat	attaccgaga	gacctacagg	gcatttagca	caacctcgta	cctcctcacg	780
aacccaaact	tggcatccat	catccatgat	gcataagcat	gttctcctgt	aaagcaaact	840
gctcgctctt	cccattatga	cggcgaatgt	attgagctgc	atTTTTgctt	ggggcaaagc	900
cgaactaaat	gcgatttcac	gcttgagagc	tttgttctat	tgcggcctgt	aatgactacc	960
gaaggaaatt	ccaccgggt	gtaccatctt	ctgaacgaag	aataggcgta	acaatgatca	1020
tctgagtgcc	ttgagcttta	aattactcat	atctgccgca	ccattcagta	caaccttggt	1080
ccggttttgt	ccaacgaaat	tttatatgaa	attactccct	cgtaagcttt	tgagcgacca	1140
aacc						1144

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

ccTTTTTTTT	acgattttcc	cggccttcat	cctcgccgct	actgctttgc	ggcttggtga	60
gggggtactg	cttcaggctc	cgatcgtagc	ctggctgtac	catcgagcca	cagaaatact	120
tcatcgagtc	cattgcggat	aagtcgggca	ggtggtggca	ttggtaccgg	cggcgagcaa	180
tccggaggaa	tacgaccttc	gcctaccgtg	atgaagcgtt	tgtccgaagc	agatgcctac	240
ttctaatagg	aggactgggg	ttcgagcaaa	gaaatctcgc	tgccattcgg	gacataacct	300
taagctccct	cttttcgaaa	tgggcaaagc	cttggcggat	gccgaagtgc	agatctccac	360

gctcctgca	cagatcattc	tcatacagac	ctcatgccca	tgatccgcac	tattggagca	420
ntgtggtagg	ggcaaaggca	ccagtcgtgc	tgcatacgac	gcgcttgagg	agctttatcc	480
aacgagaaa	acaaatggga	caaagggcac	gaccgtctca	acggacgtat	cgacagcgta	540
agagactcgt	cgataccatg	tttgccaatg	gcaaagcaga	caaagcctcg	tcataatatca	600
cccacgcntc	agctttttcg	cccaagagtt	cggcctgggc	agatcgatcat	agaggaagat	660
gggaaagagc	ctacggctgc	ccacctcgtc	gtgtggatcg	atcaggcacc	gtgccgatg	719

## (2) INFORMATION FOR SEQ ID NO:11

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

agattcagga	tgctcgctat	ctgttggtat	tcaaagtac	caaaccacct	atccgcaatc	60
ggatcacacc	ggaatcaata	accagaaaac	atataatttg	agtgtaacga	acattatcga	120
tgacgaaagg	gttactatcg	tacaagggtg	aacggcatcc	tgctgtgtca	ggaatcgtgg	180
atggcaggca	aaagcccaga	tgggaccgaa	accatcccaa	cgcgattgac	gacacggaag	240
ccgatggccg	agctcaatat	gaacgagatc	ggacaataaa	accaaccctt	aaaagtatgc	300
aaaccatcat	caccacattc	atccttttat	ttagctttgc	gaatgctctc	cctctcctat	360
tccatcttca	acgagaagcg	actgctacgc	aaggcgcagt	acagtatggc	aagctcaatt	420
cgcttttctc	caccctggct	ccatagccta	ttacttcact	tccctgtacg	aagcgtatgc	480
cacgggagtc	agttcaatac	gctatccggc	tggggcgtag	cgatcttggt	ttttgcctag	540
ccatgctctt	cttcgctatc	tataagctga	gggatgtgtg	gacgctgagc	tctatatcgt	600
acccgatcat	cgtatcgaaa	cgagcttcct	gttcaagcgg	tacgccatcc	caactatttc	660
ctcaacgtca	ttccggagct	tatcggatca	ccctcctttg	caatgcttgg	attaccttct	720
gtgtcggaat	gcccgcctatc	tcgctatcct	cttcgctcgt	atccgctcagg	aagagcgcgc	780
catgagcatc	tatggcgac	ggtagcatag	agaatgattt	tgggcaaaaa	ggctaaaaata	840
cagaccgaaa	aagttttcaa	caacgaagac	gagtttgga	tcttccaaat	aagcacctga	900
aaggaaggag	atcctgaagt	aaaaaagcag	gaaagcgaac	tttttcagtt	cggaccatgc	960
tttcaaactc	tttgcaaagc	atctgtatat	agatcaaaaa	cgattttatat	acagatcggt	1020
ttcgttttaa	tacaaatcgt	tttccatttg	tatacagatc	gtatctgatt	tatatatatt	1080
cggacggctc	aaaaggccca	ttcccgaagt	tatataaaaag	aggcacgacc	cgattccacc	1140
acgaatcgag	tgcgtgcctt	atctgtttgc	aggtctgcga	aaagttttat	cgcctatgct	1200
tcatacgcgc	tgctcgtctt	cctttgataa	gcgggtagca	tgtagatgaa	tgacccggag	1260
cgatctgccc	gggtcgttgg	tcgtatgagc	gaagtcggag	tacatgttgc	tgatcattga	1320
gtctttcggt	atgctgttct	gccggtggaa	tagctctgat	atatagccgt	tttcttttgt	1380
gtggagcttt	cctcggcttg	caaatgtagc	aaaaaagccc	aatccgatga	atcgaaaatt	1440
ttttggagaa	aaatctcatc	ctttacggga	aatcacattg	cttctgtttg	cttgcaagag	1500
cttgatttgt	aaatgccttg	agccagccga	tgtctttatt	gtatttccac	tgagtaaaaa	1560
tactcacaca	ttgagtaaaa	tgtatgggca	agtataaaaag	agctaagtac	cgctattgct	1620
ttttcctttc	tgttcggatt	attatacctt	tgagggagtt	actttttatg	cgcactctgac	1680
gatatgacaa	ccaagaaacc	ccaagccatt	ttagattaga	gaaggcctat	aacattgaaa	1740
ttcctgatct	ctcctcacaa	gaaggataag	ctggtcggta	aatagatatt	tcaagcaaga	1800
ttcctccggt	gcactcgttg	gctttgcttg	cgagaatgtc	agatagaaaag	catgacttgg	1860
ctattgattt	tctgtcctta	aaaaagcttg	atctatcgta	taaccaaatc	ataagctaga	1920
gggtctagaa	cgtcttactt	cgtaaacaaa	acttcgtcta	gaagtaacca	aatccgtaaa	1980
ctagagggcc	tggaatgtct	cacctcgcta	caaaactttc	tctctccgat	aaccaaataca	2040
gtaagctaga	gggtctggac	gtctcacctc	gttagcggag	ctttatcttt	tggaataacca	2100
aatcagtaac	tagagggtct	ggaacgtctc	acgtccttaa	cggagcttta	tctgtcggta	2160
accaaatacag	taagctagag	ggtctggaac	gtctcacttc	gttaaaaagc	ttcgtctaag	2220

agtaaccag atcagtaaac tagagggcct ggatgtctca cctcgctaac aaaactttct	2280
ctctccgata accaaatcag taactagagg gtctggaacg tctcacctcg ttagcggagc	2340
ttatctttt ggtaaccaaa tccgtaagct ggagggctcg gaacgtctca cgtccttagc	2400
acgcttgaac tatcgggtaa ccaaattccgt aagctgg	2437

## (2) INFORMATION FOR SEQ ID NO:12

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1626

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

gagggctttt attcataatt cgctcagata taaaacgaga gttaattcag tagccgattt	60
cgacgaatag tttcttccaa cattcataga tatttgccga gagtaggatt tgaccatcaa	120
ctctgattct tgtcccattt tcttacgaga gtttcacat ccatcaataa gcgtaactta	180
tccgcgaagt cttcattgct tccattggca caaggaaacc attgcgaccg ttttcgatca	240
gttcctcggg ccggtcggac aatcgtatga gattataggt agtgcatacg cttcgcttcg	300
agaagtaacca ttggtagtcc ttcgaaacgg gacgtcatta gataatagca gatgattccg	360
tagtatttgc gaatttcggg tgtagatggg attatttcta tttgcgactc catattgcga	420
gatgcaattt ctttacgtag ctcgattcat tttcgccatc tccgactatg ataagcttcc	480
aatcaggcct tctcgcagca ctcgtgatgc atcttctatc atgaattcaa aacccttctg	540
taggttaagc ctgccaatcg ccaacatttg tttgtgagta gtagcatcct ttggactgta	600
gtaaatgaaa cttgattggg tatgacatat gctttaggcg tccacgtaag attgcctcga	660
acgattgctg atctcttttt gtcagtctac aacggcatca agccctgaat acagaaaacc	720
ccttatgcgt tttgtatagg gcgggcaata tcataagaga tatgttcgca tccgatcgta	780
aatatctgcc tctgttactg atctgagaca aaattgtatt gataaaaata ttatccctat	840
caataaaacc ggttcacgct tcttgtatag ggcttttata ctcgataagc cttgaaatat	900
actgttttgc gggctaattgc attgccataa acctaattcc gagatgggtg acttctattc	960
ctttttctac ttggaaggaa gctctccttc ttttgtacaa acgctgacta atgatacgcg	1020
atgaccattg catgcagggt gttagccaag ttgatcacgg cgcgttctgt accggcacgt	1080
ttgttattgt atctaacagc agataaatca tagagaatat tttaacgttc ttttttaaga	1140
aattcatcaa ggctattggg agtattaata gcttcaatat tattgattgt aattcctatg	1200
tgaatctatt tcatttgatt gatattctggg taagcatgcg gtttggtgat cgcaatatgc	1260
atattcagct gcaaattcat gatttttttt gatattccaa agattctctt cagggatttg	1320
ccattgttgg tcattcttatt gtcttttgca gatgttttcg cccaaacctg ataaaatcat	1380
tccacctcgt tgtttttttt atgtgcgatt aaaggataat gcttttcgat acctccttca	1440
ataggcaata acacggtatt ctgaggctcg ttcttgcata gctctttatc ggagggcata	1500
atgcaactgg ttgtcgattt atatgcagaa ttaaggtctt tgagctttct ttttccttgt	1560
gaatgcgatt cttcatgcct tttttatctc tttggcttgc aattctcctt tatgtttcgc	1620
aatacc	1626

## (2) INFORMATION FOR SEQ ID NO:13

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

gcaagatatc	caaactttta	atcgggagat	tatcgctaaa	ccatatgact	aaaaattgag	60
aaggacgatg	tgctgaacat	ccttgctcagc	agtagagacc	ggagctttca	acgccctaca	120
accaagtgtt	gaccactcgt	gcactggccg	caacggctat	ggaacgaact	cgaacgaagg	180
cttcctggtc	gattcgaagg	gtacatcaat	tatcctattt	taggccagat	ctatgtagag	240
ggcctactcg	taccgaactg	gagaaggaga	tacagaagag	gattatttcc	agtgatttat	300
caaggatcct	acggtaacgg	tgcagcttca	aaatttcaag	gtgcggtttt	gggagaggtg	360
aatcatccgg	gttcgatgtc	ggtaaaagga	gacgaataac	tcttttgga	gcgatcggaa	420
tggccggaga	cctgacaatc	ttggtcggcc	gcgatcgggt	ttttgtgatt	agagaaaccc	480
gatgggcac	cgaggttttc	cagacggatc	tcagaaaggc	ccacttgctc	gcaagccctt	540
gtactatctt	gcattc					556

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1853 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

caaggctatg	ctatcctttt	cactgacaac	cggtagtgct	agcatttttt	tacagccgac	60
ggctcctaaa	gccaaagagg	ctgaggcgat	aattgcaatg	tttttttcat	ttggagtttc	120
ccttatgttt	tttatcgtaa	gtttttctat	ttggagtagg	ttttgccggg	ataggctttg	180
ccggcttctc	tacgaaggct	tgatttcgag	tagttctact	tcgaagaaaa	gcgtagagtt	240
cggctgagaa	gttcgcccac	gctacgttcg	ccatatccca	gttcggtcgg	gatacaaat	300
cgtacttggc	acccttttgc	atcagacaaa	caccctcagt	ccacccggaa	tcacttgcag	360
gaggctgaac	tttgccggct	cgttgcgaga	atagagctgt	cgaattcttt	cccttcaatg	420
ttcttgccca	cataatgaac	acgaccgtat	cctgaaccgt	cgggcgagg	ccttccccct	480
ccttcaagac	cgatacaaca	aaccgctttc	ggtagcctta	acgcccggt	gcttgcgatt	540
tcttctgat	aagctttg	tgctgccaag	ttttcggt	tgagtctgcc	tgtacttcc	600
tgaagctatt	cttgatcatt	tcgtccgcat	tttgggagag	atagcagtg	tctttcccat	660
gagtacttct	tcgaatgctc	ggagaacagg	gcacgatcca	gagaatcgcc	cggcatccgt	720
ccggtatagt	cattgaattt	attgctccgc	ttataccgaa	agcgtatgcc	acagagtcag	780
cagagtcacg	ataggcttca	cggtttgac	ctcatccttt	ttgggcgggt	ttttgcaaag	840
gcagataatc	cggccactaa	aaaggctaag	ccggcaatga	tcttactctc	ttcatagtga	900
tttgtcttct	gattatttgt	tgatactcaa	tattcgatta	taaaaatgag	cgtactaccc	960
ggtttgatat	gttcgcggc	ccacgatctc	catacgccag	atcgctcggt	atagttactt	1020
tccacttgg	cctacaggca	ttaattgaag	aatctccgtc	cagccggcta	taactccttt	1080
agagggaaac	tggccggttc	tcccctgtcc	atagagctat	cgaaaacata	ccgttgatga	1140

cggtaccgtg	ataatgacag	gttaccgtgt	ccgaaagggtg	ggtttcgggc	cctctcccat	1200
cttaatgact	tcgtattgca	agccgtcgg	aaggctcgta	caccttcctt	gtgtgcattt	1260
cttgaggga	attctctccg	gcctctttgt	tcagtttgac	agccttctgc	tgcaaatcca	1320
tgaatacgcc	tctatttcgc	gcttgccctc	gtcatacgag	agctgagggg	cttttcttcc	1380
agtacatcag	acagaccttg	catgaaatca	tccataacga	cctgtcgatg	cccgaagact	1440
tgaaattatt	accgatgctc	aatcccagag	atagctcact	ttatccatgt	aacacttgct	1500
tagttcttaa	tatgcgcgca	aaatataaat	tttacaccga	ttcctcatac	cggcacatgg	1560
caatatcttc	tgtgcacact	ccatcgga	ggcttgccgg	ttattcacag	attacggttg	1620
catccatatc	gacactgttc	ctgtgggcag	ctgtttattc	ggagccgtcg	attggcactg	1680
aagctgaaaag	cgaaagaatg	aaaaatgaaa	aaccttttgg	ggctgggtccc	ccgaatgttt	1740
tttttatttc	caagccattc	gtatgtatct	gcacaccaat	tacatgaatg	gcgtgcttaa	1800
ttttaatgct	ctctttatag	cnacttatat	tttcggaaaa	aagagctaaa	acg	1853

## (2) INFORMATION FOR SEQ ID NO:15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

tgaatatagc	cgctgccgta	ggctcgctgg	cagtaatggg	gctgacggtt	ttgtcagcac	60
caagggtg	agccacgtta	cgctgctcat	tatcggcgta	tgatcggata	tgtagccact	120
gccgtcatcg	gggtattcaa	gtttttcgt	tcgaagaaga	tattcgggca	tacgtaattt	180
gggggttggg	cagctttccc	gtgccacgga	ttcgcaactg	agtttctttg	ccattctgat	240
gttgacttta	ttccggccgg	tatgctcctt	gtcaagcagt	tgaatctctt	attgtgggag	300
aaagctacgc	acgtaatctg	ggactgaata	ctcgtcgggc	acgctgctcg	tgatctcttc	360
cgccgggttg	ctcatcgcta	ccggaacggc	ctttgcggcc	catcggtctt	ttgggg	416

## (2) INFORMATION FOR SEQ ID NO:16

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ggagaaactc	gctcgaatga	aaccgcaaaa	ccaattttaat	gcgtcggccc	gggggcaacc	60
gtcagggcg	atcgcgttta	aaaattttta	gtctctttct	ctatgatttg	aatctctgac	120
atatgaattc	gcacttggtt	gataatcggg	gtagcaatca	tgagctttag	atgcacgtta	180
gtggctgaaa	tgcgatgccc	tgatcaaaaa	tagtactacg	aaagttttgt	accttagcgc	240
gcatgaaaag	accaatctgt	ttttatctct	gctgggtgac	tttatcaccg	gtagtttatg	300
actgcctgtg	cacagaagtc	caagacgaac	aaactcaccg	aagagatcgg	agccgcaatg	360
agtatgtaca	gtcgatggat	gtgcttagca	atztatcggt	aacgtcaggc	tgtatttcgt	420
cgataccata	agtatcaaac	aatgactcgg	cgtgggtatag	atgcgatgtt	gggcgggcct	480
gacccctata	cgaatacatt	ccttacgagg	aaatggatga	actgaaattg	atgactacgg	540
agagtatgcc	ggagtcggag	ctatcatatc	gcagcgcccg	gatagtgcgt	gattatccag	600
agacctatgg	aaggatatgc	cgacagcgaa	gcaggatgat	agcaggcgac	cgcatcctga	660
ctatcgatgg	gaaagacttc	cgcaaaccac	cacaccgaaa	gtaag		705

## (2) INFORMATION FOR SEQ ID NO:17

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...854

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

ccattgaaag	gcaatccgag	atTTTTgagt	gtaaagtcgg	gcaatactcg	ttgtgtgcc	60
tatccagcgt	ataggtagaa	gtttgattat	ggccactcg	aataaggggt	gcgtatactc	120
tgctcgggtgt	tttactgaca	cgcttccatc	tttttccatt	catccttttg	gttggtgatg	180
gaaaatctat	accacatgta	tagtcgcctt	ccgagagagt	gagaacgtct	ttagaccaaa	240
ccaccgatag	ttgctgctac	cgcccggaa	ttcagccatt	accagccca	aagaattaca	300
tcgtccgcag	tagctcctgt	agatagagca	aaggctacgg	gtgacggatc	tcatcagggc	360
tgctcgtatt	gaactgtact	gtaatcgtac	tagttcataa	gaattcagat	ctgcgacaaa	420
gctgttgggg	acgatactga	gttgcccttcg	ttattatcta	ccgtgactac	gacattgttc	480
gggtctgtcg	atttacttta	atgctattga	catatcctcc	ctgtgcatgc	cgtaccggcc	540
ccactgttcg	gtgcctgtgc	gacgataaag	taggggtgatg	gtgttgatcc	ttgtgacaac	600
tgattagggtg	ccaatgagaa	actctcggga	tgctctcgta	tccgtaccaa	gagatattga	660
tagatgaaag	ttttcacctc	tatgactctc	cgtcagcctt	ggttcaatct	gtatccgagg	720
tcaagatttg	attgccttca	cctgtattat	atatcgaata	ccctacgttc	aatccggatt	780
cactttatac	tcggtttcta	tgctttcagt	gccaagatcg	gcaaggcatc	tgtccggcct	840
cagcgggagt	ctag					854

## (2) INFORMATION FOR SEQ ID NO:18

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1162

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

```

cgagacttcc attccccccg atttatatgg ataagaagaa cgccattggt attccgatga      60
tacagtctac attcaaaagcc nggacaaaat actccgagga cgtcttttca ctgcaactca      120
agatatgggt gagtacacca tattcaacat tccggcgact tactatgtga gtgaagagga      180
ggacaaatcc gccgacccat accgattcgt caaggggatc ggacagcaaa gcctgccgct      240
tctccttcat gccgagacca tcggtttctc caaccaccaa agagcaaaaa tgaataacctg      300
tacatactga ttacactttt actctccggc tttttttccg gtgtgagatt gcttttccttt      360
cttcggacaa actgcgtctt gagttggaca ggatagaggc gatctcacag gcagagcggt      420
aaacttgctg tatcgacatc cgaccaactg gtgactactc tccttggtgg taataatata      480
gttttggtag ctatggtctg ctgatggcgg gattgctggc cgcacctttg gcgcaatggt      540
tgataacgat gctatgatcg tcgttctcca atctgtctta tccactatat catactgttt      600
accggggaat ttctacccaa agccattttc aagaccatgc caatatgatg atgaggggat      660
tcgccctccc tatcgtagcg atctatatct gctttatcct ctgtctaaac tcttcaccgg      720
tttatctcgc tctttattcg tctggtggac aagaattatg tgcctacaac agtaggggtg      780
gggccgtaga tctcgatcat tatttggcag aaaatatgtc cggagaaaac gaaagaacga      840
cttgactacc gaagtgaaaa tcatccagaa tgcgctggat ttccgggtat tcaggtgcga      900
gactgcatga tcccacgcaa tgagatgata gatgtgagtt gcaaacggat attgaagtac      960
tcaaaacgac ttttatcgat ccggtttgtc caagatcatt atctacagac agancataga     1020
tgacgtagtg gatatatcca ttcgagcgaa atgtttcgtg ggcaagactg gcaaaaacta     1080
tcaatactac tgtattcgta cccggaaagc atgtatgcc aataaactatg cgactactca     1140
tgcagcgcaa gaaaagcatt gc                                     1162

```

## (2) INFORMATION FOR SEQ ID NO:19

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...584

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

```

gggaaggcat tttctctgtg ttcgatgcgt ttgcaggaac catcagcacc aaaactacag      60
atataacatc gaagcgtacc ggcagatcga tggcgacta cgcacatagt gatgcgcaga      120
ttcggaaatc agtcgccgct tgcgtgctcc acagcctctt cgggggccag tagaaagcct      180
tcggtacgag tcttgattcc acaacgacca gttctctgga cgtggatgcc acgatatcca      240
gctcgagccg ccccgactgc cagttcaggg cttctatctg atagccttgc tgccgaggtg      300
tttcagcgcg atctcttcgc cttggcgctc gcggtcgtaa tgacggccat tgctactgtc      360
gagacctttt ttttcgttcc ggctgaggat gagctctcta tgtgccgttg ttttttctct      420
tccaggatct taccacagc atgaatatgc cggtttctc cactctccg aaagactcat      480
tactgcatg ccgaaaacac gcatctccgg agacaaagct atatatgcac ttacgagana      540
gggatattga taccagctt gcgcacttct atattgagag tctt                                     584

```

## (2) INFORMATION FOR SEQ ID NO:20

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 964 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...964
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

gggtctggaa	cgtctcacct	cgttagcgga	gctttatctt	ttggataaca	aatccgtaag	60
ctggagggtc	tggaacgtct	cacgtcctta	gcaacgctga	actatcggtt	aaccaaattcc	120
gtaagctgga	gggtctggaa	cgtctcagtc	cttagcaacg	cttgaactat	cgggtaacca	180
aatccgtaaa	ctagaggtct	ggaacgtctc	acttcgttaa	caaagcttcg	tctaagaagt	240
aaccaatcag	taaactagag	ggcctggata	gtctcacctc	gctaacaaaa	cttttctctc	300
cgataaccaa	atcagtaagc	tagagggtct	ggaacgtctc	acccgttagc	ggagctttat	360
cttttgata	accaaattcag	taaactagag	ggctggaacg	tctcacgtcc	ttagcaacgc	420
ttgaactatc	gggtaaccaa	accgtaagct	ggagggtctg	gaacgtctca	cgctccttagc	480
aacgcttgaa	tatcgggtaa	ccaaatccgt	aagctagagg	gtctggaacg	tctcacttct	540
taacaaagct	tcgtctaaga	agtaaccaa	tcagtaagct	agaggggtcg	aacgtctcac	600
gtccttagca	acgcttgaa	tatcgggtaa	ccaaatcgta	agctggagg	tctggaacgt	660
ctcacgtcct	tagcaacgct	tgaacttcgg	gtaaccaa	cagtaagcta	gaggggtctg	720
aacgtctctc	ttcgtaacaa	agcttcgtct	aagaagtaac	cagatcagta	aactagagg	780
cctgaacgtc	tcacctcgct	aacaaaactt	tctctctccg	ataaccaa	cagaagctag	840
agggctctgga	acgtctcacc	tcgttagcgg	agctttatct	ttggataacc	aatccgtaa	900
gcctggagg	cctggaacgg	tcttacctng	tacaaagctt	tcgtctaaga	agtacccaaa	960
tcag						964

(2) INFORMATION FOR SEQ ID NO:21

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 860 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...860
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

ggatcccctc	ttcgatctca	acgaatacac	cgaaattggt	gaagttgcga	cacgagcatg	60
gtgacgagag	cctacaggga	aacgagtttc	gatatcagcc	aaggatccgg	cttgagttgc	120
ttcagaccga	gcgacatttt	gcgttctcgc	ggctcgagcgt	caggatcacg	gcttccactt	180
cgtcgcctac	atgcagaagt	cctgagcaga	acgcaagtgc	tgtgtccatg	acatttcgct	240



acgtgataa	gacctcaac	gccctgtgca	atctcaacga	aagcacgta	atctccatca	300
ccacaacttt	acccttcacc	ttatcgcccta	ccttaagctc	gcttcgagag	catcccaagg	360
tgaggcatc	agctgtttga	gtccgagagc	gaacgcttgc	gatcttcac	aaagtcgagg	420
ataacgacat	tgatcttctg	accagctgta	cgatttcttc	cggtatgagcc	acacgacccc	480
atgaaaggtc	gtgatatgga	taagaccatc	cactccaccg	aggtcgataa	atactccgta	540
gaagtaatat	tcttgacgat	accttcgagt	acctgccctt	tttcgagctg	ccgatgattt	600
ctttcttctg	ttgttcgagc	tctgcttcga	tgagcacttg	tgggaaacaa	ctacattctt	660
atattcttga	ttgattttca	caatctgaac	tccatcgctc	tctcaacgaa	tgcacgtag	720
tcgcgaatgg	ggcgccgtcg	atctgtgatc	ccgggaggaa	agcctcgata	ccgaatacat	780
cgacatcata	ccacccttgg	tacgacactt	cacatagccc	tttacgattt	cgttttttcg	840
agagcctcgt	tcacgcgctc					860

## (2) INFORMATION FOR SEQ ID NO:22

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...561

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

ggttaccaat	ctcaccggaa	ctgcttccaa	tgacgaagtt	tctttggacg	ggacgggtgtg	60
gaagagaaag	ctgaagagcc	ggcaagtgat	aaagcagtag	ctacaacgtc	tacaagaatg	120
gaaccttgat	cggtaataca	gctgaaatca	ttatgtggag	accggtgtag	ccaatggtac	180
atacatctac	gaagtgaagt	aaagtatcct	gacgggtgat	ctccgaaggt	ggctgtaacc	240
gtgacgtgac	caacagctca	ttgagcaatg	tagatggaca	ggctccttac	acatgcgagt	300
agaaggcaag	aagattattg	cggaagccca	tggtatgatc	acgtctacga	catcaacgga	360
cgtaccgtgg	ccgtagcccc	gaatcgattg	gatacatggc	gcaaaccggt	ttctatgcag	420
tgcgcttcga	tgtggggaat	aacaccatgt	atcgaaaata	caagtaagat	aaagcagata	480
ctttccctcg	ctaaagacaa	agaggctgcg	tcgagattat	ttttcgatgc	agcctcttct	540
tttgctactc	atgcccgtat	t				561

## (2) INFORMATION FOR SEQ ID NO:23

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...623

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

gaactcacgt	taaagtagat	tatagaaaga	cccagtaacc	caattgtaga	ctatcccggc	60
ccaactggtc	aacttttttc	agtacacgnt	caaacttttcg	gtttggcgcg	ggagcgaaaa	120
aattctcacg	ccactgcgaa	aaaattccgc	gccgcttttc	gggaaaacac	gcgccacaat	180
cggagcgttt	ctggttgat	ttccgaggct	gtcagttgta	gactttccga	caatgggtga	240
gctctactcc	tccatcctac	aggctcggcc	aacagacaag	cacgacatcc	ccaccattgc	300
cctcgcatca	gactgatgag	atcgtgactg	ttgatgcagg	aaccataaaa	aggaattttt	360
ttcggattca	tttggcgcat	aacaaaaaaa	gctacctttg	cagcgtcaaa	atcagaagga	420
gctttccttt	tgatgggtat	tactccgtag	ctcagttggg	agagcaaata	actcttaata	480
attgggtcgt	agttcgagcc	tcaccggggg	cacaaaccaa	tagcagaggg	ctgtgttgaa	540
tagttttttt	gacacggccc	tttaactttt	ggatcggggg	tcgcctttgt	gaaaggatat	600
gggaaatatc	tgtcaaatgc	cga				623

## (2) INFORMATION FOR SEQ ID NO:24

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...848

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

ggccgaagcc	cagtacaata	tggctcgcaa	cgggtgccga	cgcgaagaca	gctggcagct	60
tctgccctcg	tcgatagagc	gagaggagcc	gtcgccgagt	ggagtcgtac	atcaacgaaa	120
cctacctcat	cgccccacgg	gcaggcgagt	gtcggagata	ttcccaaag	ccggcgaaact	180
cgtaggtacc	ggcgcaactat	catgaatatc	gccgagatgg	gcgatatgtg	ggccagcttt	240
gccgtcgtga	ggatttcctc	agcagcatga	ccatgggagc	cgttctggag	actgggtgcc	300
ggctctgaat	gaagaaaaag	tacgcttcaa	gatcacattc	atcagaacat	gggtacctat	360
gctgcctgga	aagcgaccaa	gacaacaggg	catacgacct	gaagaccttc	gaggtaaagg	420
ccacccttgc	ggataaagac	aggcacaana	gctacgcccg	ggtatgtccg	tgatcatacg	480
caagtaacga	gagcagtaag	gccatgcacg	ggacagccct	tatagccacc	atgcgtagaa	540
ggtgcgacaa	ctgacgagtc	gcgtcctctt	cctcttctgc	atgggtgatg	tcctgtcttt	600
tgctgtctct	tcttcccttc	catcatggat	atgggggtgc	gcagaacctg	cctgcgggta	660
ttgtggatct	cgatcgtaca	cagacgcgcg	caccatagca	cgccacctca	attcgatgga	720
gcaaacccaa	atcgtaaaac	gttcgaaggc	tgcgtagagg	tcgcttgagc	tacagcgagg	780
cgagtatcgt	actactatat	acccgaggaa	tgacacggat	gcctacgcac	agagcagcca	840
agctctct						848

## (2) INFORMATION FOR SEQ ID NO:25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

```

ggcggcgcaag tagtccgaag ccgaggggat accgctcgct cctccgtaaa aatctccgaa      60
ggcaggctcgg ctccgcttcg ggatcatttcg tcgaggaatc atcgatgagc gagaaggcgt      120
ccggctcctt ttccggccgag gcgggttcag ctgctccgga tgcgtatatt gctccacgag      180
caggtacagc ttgcgctgtc cggcagatag ggtgccagcc ggcgcagctc cgaagcatag      240
cgcaactcctg caccacatac atattatata ggtataggaa gacgaagggtg gagcgtaggg      300
ataggcctcg tacagggtct tcatctcggg cagcgtgtca gccaaagccg cgaggggtgc      360
tccatgtagg cgtacagatc gttagtcgtc atgtggggga ggattaccag ttctctaccg      420
tagcgttata cacctgcttc acaagtcgtc gaccatattg gccagcaggg cgtcttgtag      480
gtccaccagc gctcgtctgt gtcgaagtcc gtggaagacg taaagtcccg atcgaagttt      540
gttcggggagg ccttggttct gtagtgcaac tgtatggata aggttacctg gtgcgtgcgg      600
ccagatcggt ttctctgtac gcgaggggag cgaagtctaa ttagtgatga ccacctcgat      660
gatcatgtcg gcatcggttg ttctgtcatt tcgagcttgg tacggcgcgt aaaatgggtt      720
tggagggtct cgggtctagc tgcgccaacg ggggatatac gcgggtggcc tgattgggtc      780
catcggcata taaagcggtt tgatgcggct atagtccaga gcacctccgt tgagctgtag      840
gagatgctgc atgccgagca ggtcagcagg acgataagca ccccgcaaga gcgaaaaggc      900
tgtatcgccc gagggttcta ttccagtcca tctccttgat ttacgggtat agtgtccgct      960
ccgaaatcct cagttcctcg ctgtctgctt gcgccttcgg ccgtggcggt ccaatgcaag     1020
ggaaatcatt tcttctctac ctccctccagc gaaaccggat cctcggtgta ttcgctgggt     1080
cctgtatcgg ctccacgggt tctgcccgtc tcgcgatggg ggccttggcg tgctgacgcc     1140
ccacttcgga tctgcgggtc gcttgctgct gttgccaga cgtccgacct tacaggccat     1200
gagggctggt cgtgggtgcg caggcggtta tcatcccctt caaatcggct atctctttct     1260
tcatatcgta tagccctggt agatgatttc gcgctcgtaa tgggggattt gtttgtccgc     1320
ttcgctggtt cgttccgtcg gatcacgacg ggggtggagg cttgcatccc cttagcgtcca     1380
ggtagcagag gatgggtctc gccgataccg tccgctcctc cccaggatgc tcagcctgtc     1440
ggttatattg cgcagctctc gcacattgcc ggccagcggg aacgcattaa tatggtacgg     1500
gcttcgtccg ataggcgcac ggaggcatcc gatacttctc ggcgctgtcg gcggcgaatc     1560
ggcgaaaagc aagggcacgt cgtccggctc catacgcagc gcaggcacct cgatcggacc     1620
gtattgagcc ggaagaagag gtcttcccgg aacttcccgt tcgctacgcc tccttgaggt     1680
tcacattcgt cgccgctacg atacggacat ccgtctctgc gactggctgg ctctacggg     1740
gatgaactcg cccgtctcca gcacctcagc agcctcgctt gcgtgggcaa aaggcagttc     1800
gcccaactcg tccgaaagaa tcgtgccgcc ggatggcttc ttcgaagtac cccttgcgat     1860
ccgata

```

(2) INFORMATION FOR SEQ ID NO:26

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 632 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

cgaaacagct	gaagcattgt	cgcgtacgtct	tcgtttttggc	attcgtccta	tcacgttctt	60
tgaagagttg	ctctgctgcg	gcaaactctt	cgggcgagtg	gaacccactt	cttttttcat	120
cgctccttg	gcctcttcaa	gtgtcagtg	ccttcgcgat	gagcctcttt	gatgtcgagc	180
atagctcca	acttactttg	tcgagggtgt	caaaagtctt	atttgttttt	atgacctgca	240
tgtttttgag	caattagtga	tgaataacaa	cctcctcgca	gcttatcaaa	agctattgtg	300
gaggtatata	cactttcgt	aatataacaa	tctcagaata	tattttgttc	tgggttttca	360
tcgaggaaaa	aagtgcata	gtcattacg	cccaagcagg	atacgagcct	gaaatgctcc	420
gattgtggtc	tgtgttttgt	gaaagcaggc	gcgagatttt	tttcgttttg	gtttcacttt	480
ttttcttttc	cacgccaata	gcaaaaagtt	cacgtgccac	acttttggtg	gtcataaacc	540
gaaaatttag	gcgtgtgaac	ccaatcggat	agggatgata	catcctatgc	tgaatcgga	600
gtgaatatgg	tgcaaaaaaa	gagggacagt	gc			632

## (2) INFORMATION FOR SEQ ID NO:27

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2331 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...2331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

gcagatgcta	cgcccgaat	agacttttgt	gtccttgtgt	gcgcagctat	ggaaagaatc	60
atcttcta	tttggaactg	ttcagcactg	catcttat	ggtgtagaaa	aaccagggtt	120
atgaaggctt	taccctgaaa	atgtcaaga	aaatccggaa	ggatgtaatg	aagccaaaga	180
cttcttcctg	cgcacgagt	aggattcaaa	gacttgatcg	tcacagagca	acctctttcg	240
aacgagtact	caaggaaata	ccggatgaat	tgaagaatt	catattgaaa	gaatcgatgg	300
ccgaagcgta	ttagaaatca	aaacttctca	ttgggtatat	gacaagacgg	taatcaggtc	360
gaggaaaaaa	ttttcgccaa	ggatgaaatg	gatcggaagg	aaccaagaaa	gtcatagagc	420
tttcaggccc	tttattcgac	aattgaaaga	aggttctgtt	ttgctgatag	acgaattaga	480
tgccaaactc	accccccttt	gaccagaagt	attctgaagt	tgtttatgtc	tccggagaca	540
atcccaatgg	agcacagtgt	atctttaata	ctcacgacac	aaatctgcga	agggcgatta	600
tttacgccgt	gatcaaatct	ggttcacgga	aaaagacgga	cagaatcctc	cgatctttat	660
tcattgatag	agtttcgaga	tgacagagg	taaaagtctg	taaagatcgg	agttttcaaa	720
acgactatat	taacgacgtt	atggagctat	cccgttcatt	ttttcaagt	tagagccatg	780
ggacaccacc	aaaaagagaa	atagaacgac	taaaacgtga	aaagcgagaa	gcaaagccgc	840
aagaaaacgc	aaagagaata	cccgggacat	aatagttcga	ttctgatcgt	ttgtgaagga	900
caaaagacgg	aacccaacta	ttttaaggct	tgattgacaa	ccactactcg	gaagttcgtg	960
aggcagagat	taggggacaa	gttggtctac	ttgtgcatta	gtcgaacgag	ccaaagagat	1020
tcgggataac	tcgaaaaaga	gcgtgaatta	ggctttgatc	ggatttggtg	tgtctttgta	1080
aagacgattt	tgatgatttt	aatcaagcta	tcgaccttgc	aaagagcatg	gtttcggatg	1140
cgcttgga	aacgaagctt	ttgaattgtg	gttcctctcc	atttccaata	tctggatgta	1200
cctatcagcc	gtgatgctta	catttcaaac	ttgaaaaact	gatacaaaag	cgacttaatg	1260
ataattcttt	ccgaacaata	agaatgatcc	ctccttttac	aacatattga	aagaccatgg	1320
agaggaaattt	tagcaaagcg	atatgccgaa	aaacttcgct	tgaaacacaa	ggtaaagatt	1380
atgctaata	caacccctgt	acaagggtcg	atctattggt	taggaattgg	aaaatcccct	1440
gtccgtatta	aagaacaaat	aaagagggtg	agatcactca	gggcaatcgc	acttgaactc	1500
ctaattgtacg	tatagcttct	gattgctaca	ttcaattatc	aaaacaagca	cgaattcata	1560
tctcagggtt	caaattatag	agggaaagaga	ctgaaaaatt	ccaaaagaga	tcgctccaat	1620
ctccctgacg	gactgcaatt	tatttgta	tttgtagcta	acgttggttg	ttgcaactat	1680
ttcaaacaga	tgagagcaaa	catttggcag	atacttcgct	ttcggttctc	ttttcttcg	1740
ggacagcgat	cggacaggct	cagatcgaaa	ccgtacatac	gaggcttatg	tgaacagta	1800
cgccgacgaa	gcttccgaca	gatgagccgc	tacaatatac	cggcaagcat	caccatagca	1860
cagctttggt	ggagacagga	gccggagcca	gtacactggc	cagcgtacac	acaatcactt	1920

gggatcaaa	tgccacaaat	cgtggacggg	caagcgacc	atcgtagcga	cgatgcgccg	1980
aacgaatgct	tccgcagcta	ttcggccgcc	gcgaatcgta	tgaagatcat	tcccgatttc	2040
gtcccaacc	acgctatctc	ccctgttcaa	actcgacaga	gaagactatc	ggggctgggc	2100
cacggggtgc	aacgctgtgg	ctatgccacc	aatcggggct	atgccaatct	gctgataaga	2160
tggtggagct	gtatgagcta	tatgctttgg	atcgcgagaa	gtaccctcat	ggttccacaa	2220
gtcttaccct	gggtccaaca	aaaaatccca	tcaacgacca	agcagaagca	gagcggactc	2280
aagcacgaag	cttacttcaa	gctccggact	ggctctacat	cataagccaa	g	2331

## (2) INFORMATION FOR SEQ ID NO:28

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...784

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

gcgtacgacc	ctttcgatgg	ggcataaaca	acgaaagaaa	acgagacaaa	acaaaaaacg	60
aatatagaat	tatgggaaaa	atcattggaa	ttgacttagc	acaacgaact	cttgtgtctc	120
tgtattggaa	ggtaacgaac	ctatcgattt	acaaacagtg	agggcaagcg	cacaacgccc	180
tcggtagtgg	cttttgggat	ggtggcgagc	gtaagggtgg	cgatccggcc	aagcgtcagg	240
ccatcccaat	ccgaccaaga	cgatatactc	tatcaaacgc	ttcatgggcg	aaactacgat	300
caggtttcca	gagaagtgga	gagagtgcc	ttcaaggtag	tactggggac	aataatactc	360
cgcgcgtaga	tatagacggg	cgtctctata	cgcgaggaa	atttcggcca	tgatccttca	420
gaagatgaag	aagacggccg	agactacctc	ggtcagggaag	taacggaggc	cgtgatcact	480
gtgcccgc	cttcaacgac	gctcaacgtc	aggcaacgaa	agaagcagga	gagatcgccg	540
cctgaaagtt	cgccgtattg	tgaacgagcc	tacggcagct	tctctggcta	cggtctggac	600
aagtccaata	aggatatgaa	gatcgctgtc	ttcgactggg	tggcgggtacc	ttcgatatct	660
ctatcttgg	attgggagac	ggcgtttcga	agtgaaatcg	accaacgggtg	atacgcacct	720
cggaggagac	gacttgacca	cgtgatcatt	gctggctggc	agaagagtca	agtctcaaga	780
aggt						784

## (2) INFORMATION FOR SEQ ID NO:29

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...545

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

gcgagtttac	ggaagtaggt	gctgatatcg	aagttcaggt	aatcgagatg	acaaggaaaa	60
ccgtcgtctc	agcttgggtc	acaaacagtt	ggaagagatc	cttgggatgt	attcgagacg	120
gtattcactg	taggatctat	ccacgaagaa	cggtaatcga	agtgatggac	aaggggtgctg	180
tcgtttctct	gccttaggtg	tggaaggttt	tgccactccg	aagcacatgg	tgaaggaaga	240
tggtacaggg	ctgtactcga	agagaagtta	cctttcaagg	ttattgagtt	caataggatg	300
ccaagcgaat	cattgtatct	catagccgtg	tattcgaaga	tgacagaaaa	tggtcagcg	360
tgaagccaat	gcagagcgta	aggctgaagc	caagcggctc	agaaagaagc	tgctgccgaa	420
gctgccaatc	ctgcacaggc	ttagagaaaag	ccactctcgg	agacctcggc	gagctggccg	480
ctttgaagaa	gcttcagaaa	ctaaaactac	tacggatcat	acgcgctttg	gcgtatgatc	540
actta						545

## (2) INFORMATION FOR SEQ ID NO:30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...849

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

gcctgtatct	gttcgctgcg	tgctcctttg	agagccttgg	cgttctgagc	tgtgcagctg	60
cttcggcagc	ctttgcctgc	tccatcttag	ccgctacgcg	ggggcttcga	tgacagcgag	120
ggatcgcgg	gcctgcacct	gctgtcctcg	gataccctaa	gttccttgat	gcgcccgggc	180
actttgctgg	acactcgtat	tcggtcactt	ctatctgtcc	ttggataatc	tcctcggccg	240
gtctggcatg	aaaaaaccaa	cgatcgtcac	cactgcgatg	actcccagca	agagagaaac	300
gccgggaata	cgatattacg	ttgtttgttg	tccgtcataa	tgaaatatgt	ttgatcagat	360
gaataacgaa	ataaggaaaa	acggtatcat	tcgaaacgac	ttcttcgggg	gagaggtgtc	420
ccgaagcctt	gcgcagcatc	attcggtcag	tttcacgtcg	atctgtgcat	cgatccttgc	480
agaccggggc	acaaccatgc	cgtctgagct	tccagtacgt	tgaggccgct	tattacgcct	540
cgcgaaaacc	tacattggca	tagcgcaggt	tctcttcggc	tttcttcctg	tcttcgtggc	600
catgacaagt	cgtttgctctg	cctcccgtac	tttcaggcgc	tttgggagag	ctgtagctcg	660
atgctttcgc	gtgctttggc	aagttgtggg	ctgcgatgcg	tgccctcggt	ttggccgctc	720
ttaccttatg	cgtgcctgcc	cccagtgcca	gataggaact	ttgagcatca	caccacatt	780
ccactacctc	cgaattattc	tcgaaaccat	tgaaagagga	cggattagtc	actaatagtt	840
tggaacga						849

## (2) INFORMATION FOR SEQ ID NO:31

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...2843

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

tgggtacggg	caagaccact	ttcatcaaag	ccgtatgcga	ggagctgggg	tctcggacgt	60
tatcaatagt	cccacctttt	cgattatcaa	cgagtaccct	cggatcagac	gggccaactg	120
atctatcact	tgcactgcta	ccggctcaca	agatagaaga	cggcctgaat	ctgggtgtag	180
aagactatth	cgatagggtg	gtctctgctt	tatcgaatgg	ccggagcttc	tggagccgat	240
actccgaacg	atacggttca	tgtccgaatc	gaagagctgg	aagacggcaa	gcgcggctta	300
catttctaag	cctgctccga	tgtcgttcgt	cattcggggac	ttcatctcat	cctctttgcc	360
atagtcggtc	tggtttcgct	actgactgct	ctctctgtcc	ggattggcta	ctgagcagcc	420
gaggcgacag	catttggtatc	atgccttcgg	caagcgaggc	gcacgtatct	tctatattat	480
aataggagtg	ccttgctgag	tgtcgcggct	ttcgggctga	tcaaactctg	aaaagtgtct	540
gcagtaaaat	cgctcatcata	aaagagaccg	cccctgctca	gcctcatttc	gtatattcct	600
tataacctct	tcaaggggaa	acctctacct	ttacggtgga	atcaatttca	gaccgatgga	660
ttacgaaata	gagaacaacc	atgccgcagt	attcgcaggg	gaagtatcga	agtgatatgc	720
ggctccatgt	tcaagtgcgaag	acggaagagc	tgtctacgcc	tctgcggaga	gctaagatag	780
cgcgacagag	gtggagatat	tcaagccgac	catcgatata	cgctacgacg	aaaggatgtc	840
gttttcgcatg	acaagaatgc	tatcgcttcc	accccgctgg	acattcggcc	aataactatgc	900
tgtatctctc	ccaagtggat	gtggtgggga	tgacgaagcc	cagttctttg	atgagggtct	960
tgtggaagta	gcccagcaat	ggccgatcag	gggtgttcgcg	ttgtgatcgc	cggattggac	1020
atggactttg	acgtcagcct	ttcggaccta	tgcggggctt	gtgtgccata	gccgactcgt	1080
gaccaaagtt	catgccgtgt	gtgtggaatg	cgcccgattg	gccagctttc	tttccgtcgt	1140
gtccaaggcg	atcagcaagt	gatgctgggc	gaactgacga	atacagtcct	ctctgcagaa	1200
cctgctacag	gaaatgcagt	tctccccaca	aacagaagaa	atccattcga	caatatgaat	1260
agcagacatc	tgacatcaca	atcattgccg	gcctctccct	ctttgtactg	acattggggcg	1320
gctctccgta	gcccacaacg	atacgcagtg	gactctcggc	ggaaagctct	ttcttcggcg	1380
tggatacaac	gttcggccga	atatcaagcg	ctttgcattc	agcatacaac	atcgctacgg	1440
aaagagtggg	cgctctaccg	gcagaaccta	acaaggagat	aggccttatg	ccatcgtaac	1500
ggacatagac	gaaaccattt	tggacaatac	gcctaactcc	gtgtatcagg	ctcttaaggg	1560
caagattaga	tgaagagact	tgggggaaat	gggtgtgcaca	ggccgatgcc	gacacacggc	1620
aggagctttg	tctttcttcc	tccatgcagc	gaacaagggg	atcgagtctt	ttacgtcacc	1680
aaccgcagag	acaatctgcg	cgaagcaact	cttcaaacct	tcagcgttac	ggattccccct	1740
ttgccgatga	agaacatttg	cttagaccca	tgggccatcc	gacaaagaac	cccgctcggt	1800
caaaatacaa	gaaagtatga	aatagtattg	ctcataggag	acaacttggg	cgacttccac	1860
cattcttcaa	tacgaaagaa	gagtccggac	gcaaacaggc	tctgggcctg	aagccgggga	1920
gttttgccgg	cacttcatca	tgtgcccaca	tcccaactac	gatcttgagg	accggcatgg	1980
tacggcgagg	agtatccgcc	actgcccga	gagacaaagc	acttaaaaca	ctgcaactcac	2040
agaacagcag	atagctccta	agcaaacaca	tccaatagac	agactcacac	tatggacaac	2100
aaacgacaag	caaaatagaa	agactgctcc	agaaagaact	cagcgagata	ttcctggggg	2160
tgcgaaatcc	ctgcccggcg	taatagtthc	ggtaacgaac	gtacggtaag	tcccgaacct	2220
agcatcgcac	gtatacacct	gagtatactc	ccatcgagaa	gagcagcgag	attcttgaga	2280
gcatacaaca	caatacaaa	acgtccgtta	tgacctcggg	cagcaagttc	gtacccaact	2340
gcgcaagata	ccgatttgac	attctacata	gatgactctc	tggattatct	ggagaatata	2400
gccgtttgct	caatcaataa	gaaacggtcg	ctctctatca	agacgctgtg	acttccccctt	2460
tttcatagcc	cgccgttact	tgttctcccc	caaaagatta	gtgcgggtcaa	tgtggtttcg	2520
ctcgtttcga	cgaatagctg	ctgcgtggct	cttcggcctt	ggtttgatc	ctctctatth	2580
tcaatgggta	cgaagcttga	tcatgacgca	ttcggcagta	acggatcccc	ctcttatgat	2640
tcggttcgcag	acaattcgct	gataaaggca	gatgataaaa	ctctgctcac	agctccgaag	2700
cggaagggat	cggttcgtac	agctttatcc	tcaccggaga	aggtttgtaa	agacgaagta	2760
tcgacagcag	gctgtttctc	tcatgggtgt	ggagatcgct	atccccgcac	tgtgaagata	2820
gactccatcg	tctttgcagg	caa				2843

## (2) INFORMATION FOR SEQ ID NO:32

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 881 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

tccaggacgg	atacgccgca	tagctcccaa	ccatgcctct	gtgctgatcc	ggccgaagag	60
cggtagcggc	aaagagttga	tagccgaagc	tctgcacctg	ggagcaaacg	agcctcagcc	120
ccattcgtca	agggtcaattt	gggtgggttc	ccgaaagt	gttcgaaagt	gagctgttcg	180
gacataagaa	aggagcttta	ccaatgcttt	ttccgacagg	aaaggacggt	tcgagctggc	240
tgatgcggca	cgatctttct	ggacgaaata	ggcgaaactac	cggtcggcaa	ccaataaaac	300
tgctgcgagt	gctacaggaa	cagacattcg	agccgttg	cgaagcgtct	cccaccgagt	360
ggacatccgt	gtggtatcgg	ctacgaatgc	ttcttgagc	gaatggtagc	cgaaggacgt	420
ttcagagagg	acctctacta	tgaatcaacc	tgatacatct	gcattctgcct	ccgctgcgtg	480
agcgtcagga	gatatacagc	tgctggtgga	agccttcagt	gaagcctttg	cccaatcgac	540
ggattgcccc	atgccgtttg	gagtgcggaa	gctatgcgac	gtatctgtcc	atgcccctac	600
cgggcaatgt	acgcgaactg	aaaaacgtag	tggagcgacg	ctattgctct	cgggatcgag	660
agaaatcagt	gcccgggatg	tggctgcttc	ggttcgcagg	tgacggcagc	agaccactcc	720
gacgaacggg	ctttgccgac	atggaggaag	ctgctatccg	agagacgctg	actaaataca	780
acggaacggt	agtcgtgctg	cacgagcctt	gggattgagc	cggcaagctc	tttcgggcga	840
atggagaaat	acggactgtg	atagtgtgta	aaacagaatc	g		881

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

cctctgcttc	ccgtacagcc	gtatgtgcc	aaagcgagaa	gcctgtaatt	cacctgcagc	60
atagacattg	ggcaggggaa	tttgcatect	ctcattagct	ttacaccttt	gccggcaagc	120
accaatccga	gcgactcgaa	tccttgcgca	cggggcgacg	tcccacactc	atcaggatac	180
gttctccttc	gatctcttgc	tttctccttc	gtattctacc	gtaacagctc	cgttgcggaac	240
cgatgtactt	tgtgcccag	gtagaatttg	attccttctt	tttcatagt	agcggtagca	300
tagctgcatg	ttcgggatcg	ataccgttga	gtatttccgg	cagatctcca	ccacgtgcac	360
ttgcgtaccg	ataccgttga	agaaagaagc	gactccattc	cgatcactcc	accaccgatg	420
atgacgagag	aggtcggaat	cctttgttct	gtagagcttc	acggtttgtc	caatactctg	480
tctgctccac	ccgggggatg	gtggaataaa	cgtctccgaa	ccggtacata	gtagcagggtg	540
gcagctttgt	actgtgcttc	gcccgagtaa	tgccgatgat	gccgtctgat	cgcaccccg	600
acggtagctt	ctgccgtcac	atctctactc				630



## (1) INFORMATION FOR SEQ ID NO:34

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1353

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

tcggcatttt	cggttcgaaa	atccaagttt	ccaaccaanc	cacagacttg	atcgctcccc	60
tttgcatagc	aaatctgtga	ctgccggttc	atccggaaca	ggaaactttt	ttcttggtat	120
cgttcaagaa	cgnaaagtct	gtgccgacga	ttggcacaag	tccttcccgg	cctgttagag	180
attgaggact	gtcagcaatc	ggactttcgc	atcggtcatt	atgacagacg	aggaagtatt	240
gaacaccgcc	aaacggtcat	tgttatgctt	aaagggataa	atccgaatcg	tgcgcacgat	300
aattgcaata	cgtagttaga	gatggcatac	gactttacac	aaaattccgc	aacagcctgg	360
agtacagcta	tcaggaagca	acccgtctcg	gctcgtagcc	gtgacgcaag	atatgctcgt	420
actcggtatc	attcgcgacg	ggacaatggc	gcgatcgaca	tcatgcggca	ctatgggatc	480
aacttgtagc	actcaaacgg	ttgatcgagt	tggaagccat	cgccgagagt	ttgcctgctc	540
gcctgagggg	tcgcccattc	tcaccccttc	ggctcgggag	gctatcgaga	tgccacagac	600
atctgtgccg	acatggagga	cgaggccgtc	agcccgggcca	tctgttgctg	agtatcctca	660
actcgacaca	ggagagctta	gtacaaagat	atztatgaaa	caaggtataa	aatacgacac	720
catcctgtcg	gattattcgg	acagcgcaac	ccctccgaag	ggaagtctcc	ctccgaaatg	780
gagacctcga	cgggtaccaa	gacaacgact	tcgacgacga	agaggacgaa	tccttccgcc	840
ttccgggaat	agcgggacag	gcggaggctc	cggcgacgcc	ccgaacagaa	taccggcgga	900
ggcgatacta	ccaccacgac	acggagtggg	gcgacacgcc	tgcaactggg	accttcggga	960
ccgacatcac	tgccatggcg	cagcaggcaa	gctcgacccg	gtagtgggtc	gggagcagga	1020
gatcgaaaag	tgatacagat	actcagccgg	cgcaaaaaga	acaatccggt	gctcatcgcg	1080
aacccggtgt	atggcaagag	tgccatcggt	gaaggactgg	ccgaacgata	gtgaacagga	1140
aggtgagccg	tattcttttc	gacaagcgga	tcatacctc	gattttggct	cagatggtag	1200
ccggcaccaa	atatcgcgga	cagttgaaga	gcgggtgaaa	gccgtgctcg	atgagctgaa	1260
gaagaatccg	cagacatnct	cttcacgcac	gagatacata	ccatcggtgg	gaagcaggct	1320
ctgagccgga	tcgatggata	ccgtcaatat	gct			1353

## (2) INFORMATION FOR SEQ ID NO:35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...467

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

ccggagagag	acgtttttcc	ttcgaaaaga	taactgccat	ccccaaaac	ttaaagggga	60
gttcttcttc	atcgtaactc	tccgtaatct	cgccgacgtc	tcttcccaat	atgtcctcca	120
ttgtgatcag	tccgcaagtg	ccaccgactc	atccacaacg	atggagacat	gcaccttatt	180
ggctctgaac	tcctcggaac	atcatctatg	cgcttggttt	cggggacaaa	atatgcttta	240
cgaatagagg	atgccagtcg	aattcatcgc	ctttatccat	gtgtgggatt	agattttgat	300
gtaaatcacc	cctttgatat	tgtcttctga	cccctctgaa	acggaagtct	ggaataaccc	360
gacgaaacaa	cgaagtcaag	catcttacga	aaggccagct	cagatccaca	tccacaatat	420
cgatacgcg	gaaccatgga	ttcgcaggct	ggcttattat	aggaatt		467

## (2) INFORMATION FOR SEQ ID NO:36

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...452

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

gccatacctg	tccgattggt	gcggctgtag	tccaaacgct	gaatacaact	ccgcttgggga	60
tgtagtactt	ggccgtagtc	aatttgatca	cgccgttgat	ggtagctgac	gagtcgtttg	120
tacaagccct	ttgccatagc	tcttttgccc	atcagtacag	ccctgtccat	atcctgcagt	180
gctccggcta	caatctcgag	gaagatgccg	attgtccatc	gatcaggact	actatcggga	240
gtttctgtcg	atcggttcag	tcaatgtgcg	aaatacggac	gccgactntg	caatcgacct	300
ttggtcgtta	ccacctcttt	gcccttaggg	acgaacagat	tgatatctcg	atagcagcct	360
gcatcagtc	gccaccattg	ccttcttaaa	tcaaaatgag	acctttcgct	ccttgtttgt	420
nacgaagatc	caacaaggcc	ggcgcacctc	tt			452

## (2) INFORMATION FOR SEQ ID NO:37

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: UNKNOWN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1157

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

qtattgaagg	tcgtatccct	tggtcgctat	cacatccctt	ggcttcatcg	taaggacgag	60
tcgtatccg	gcacgatgga	tgcgcgccaa	gacggcttaa	gctctatgtc	caccatccgg	120
cgaatctccg	tcttgcccag	ttggtcgaga	ggatgatatc	gtccaaacgg	ttgagaaatt	180
cggggctgaa	cgtcttttca	gagctttttg	gatcacggaa	cggctatgct	ccttgttcgc	240
ttcctgtctt	tttccgaacg	gaacccgata	ccctgcccga	agtctttgag	ctgggtgtac	300
ccacgttgga	ggtgatgatg	atcacggtgt	tcttgaaatt	caccgccgtc	ccagactgtc	360
ggtcagctga	ccttcgtcca	tcacctgtaa	gacagattga	agacatcggc	atgcgccttt	420
tcgatctcat	ccaagagaa	ccggaatagg	gtttgcgtct	tacgcgctcc	gtcagttggc	480
cgccttcttc	tagcccacat	atcccggagg	ggcaccacg	agacgcgaaa	cggagaactc	540
tccatatact	cgtcatatc	cacctgatc	atggcattct	catcctcgac	aggtattcgg	600
cgaacttctt	ggccaaatag	gtcttgccca	cccccggtgg	ccgaggaaaa	ggaaagaacc	660
gacgggtttc	ttttcattgc	gaagtccaga	cgattgcgct	ggatggcatg	caccatcttt	720
tcgatggctg	tgcccgacct	actactttgg	tcttgagatc	atctgccatc	gtgcgcagac	780
gttcccttcg	cccggtctca	gccgctcagc	cggaaacgct	gtcatcaacg	ccatacatgc	840
gccactacat	tctcgtccac	cgtctcgcgg	tgcttggaca	tcgctcttcc	cattttttct	900
tctcttccgc	tatctgctgc	tgagtgcgcc	gtcctgatcg	cggaaaggagg	cagccagttc	960
gtagttctga	gccttttacgg	cgagagcttg	ttctctcgca	ccgatgccaa	ttcggcctcc	1020
agtatctcgt	ttcttttcgga	gccaccacat	tggtgatatg	gacgctcgcg	ccggcctctc	1080
catggcatct	atcgcttat	ctgggaagaa	acgatcggat	acatagcatc	ggtcagttcc	1140
actgccgctt	tgatcgc					1157

148